



Plant Archives

Journal homepage: <http://www.plantarchives.org>

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-2.072>

ASSESSMENT OF GENETIC DIVERSITY IN FIELD PEA (*Pisum sativum* L. Var. *arvense*) FOR YIELD TRAITS THROUGH MAHALANOBIS D² ANALYSIS

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(Date of Receiving : 09-03-2026; Date of Revision : 23-04-2026; Date of Acceptance : 17-05-2026)

ABSTRACT

Field pea is one of the important rabi pulse crops that requires improvement to enhance productivity due to its growing demand. The present investigation was conducted to assess genetic variability, heritability, correlation, and path coefficient analysis among fifty-seven field pea genotypes during the Rabi season 2024–25 at JNKVV, Jabalpur, in a Randomized Complete Block Design with two replications. Genetic divergence analysis using Mahalanobis D² statistics grouped the genotypes into eleven clusters, indicating the presence of substantial genetic variability. Cluster IV exhibited the highest intra-cluster distance, while the maximum inter-cluster divergence was observed between clusters V and VII, suggesting their suitability for hybridization programmes. Among the traits studied, biological yield per plant (31.52%), plant height (25.69%), and harvest index (10.78%) contributed the most towards total genetic divergence. Cluster mean analysis revealed that Cluster X was superior for seed yield and several yield-contributing traits, whereas Cluster VI showed higher values for harvest index and related attributes. The results indicate that selection of genotypes from genetically diverse clusters, particularly clusters V and VII, can be effectively utilized in breeding programmes to improve seed yield and associated traits in field pea.

Keywords : Field pea, Genetic divergence, Mahalanobis D², Cluster analysis.

Introduction

Field pea (*Pisum sativum* L. var. *arvense*) is one of the most important pulse crops cultivated in India, primarily during the winter season. It is an annual, herbaceous, self-pollinating legume extensively grown across temperate regions. Field pea has a diploid chromosome number of $2n = 14$ and a genome size of approximately 4.5 Gb (Arumuganathan and Earle, 1991). The crop belongs to the family Fabaceae, the largest family of flowering plants, which comprises about 450 genera and 1200 species (Luitel *et al.*, 2021). The genus *Pisum* includes two species: *Pisum fulvum* Sibth. and *Pisum sativum*. According to Vavilov (1949), the primary centres of origin of field pea are Ethiopia, the Mediterranean, and Central Asia.

Globally, field pea is cultivated across a wide range of agro-climatic regions, with major producers

including Canada, Russia, China, and India. In India, it is primarily grown in Uttar Pradesh, Madhya Pradesh, and Bihar, with Uttar Pradesh being the leading producer. Due to its high nutritional value and adaptability, field pea is gaining attention, however, its yield potential remains limited. Breeding in field pea faces several challenges that limit genetic improvement and crop productivity. One major issue is the narrow genetic base due to domestication and reliance on a few cultivars, which restricts the introduction of new traits such as disease resistance or stress tolerance. Lodging, pod shattering and poor synchronization in flowering and maturity further complicate breeding efforts, affecting yield and harvest efficiency.

Genotypes exhibiting desirable traits can be grouped using hierarchical clustering to quantify genetic distances among clusters, thereby aiding in the

identification of genetically divergent parents with greater potential for improving target traits.

Material and Methods

The Experimental materials consist of fifty-seven field pea genotypes including two checks received from Department of Genetics and Plant Breeding, College of Agriculture, JNKVV, Jabalpur and IIPR, Kanpur. The experiment took place during the *Rabi* season of 2024-25 at the Seed breeding farm, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh in Randomized Complete Block Design with two replications. Each genotype had been sown in 5 meters row while plant to plant distance was 8-10 cm and row to row distance was 45 cm. From each replication, five plants were chosen to record observations on various traits, including days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, plant height, number of nodes per plant, number of effective nodes per plant, pod bearing length, number of pods per plant, number of effective pods per plant, pod length, number of seeds per pod, 100- seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g).

Results and Discussion

Genetic Divergence Analysis for Quantitative Traits

A total of fifty-seven field pea genotypes, including two check varieties, were analysed for genetic diversity using Mahalanobis D² statistics. Where the average values of related traits were converted into standard, uncorrelated values to calculate D² values. For each pair of genotypes, the difference between their uncorrelated trait values was squared and added up to find the genetic distance between them.

Contribution (%) of Individual Traits towards Genetic Divergence

Table (1) shows the proportional contributions of each of the sixteen quantitative features under investigation to genetic divergence. The traits with the largest % contribution to the overall deviation was found of biological yield per plant (31.52%), followed by plant height (25.69%), harvest index (10.78%), pod bearing length (6.20%), low per cent of the contribution demonstrated by number of pods per plant (4.89%), number of effective pods per plant (4.64%), seed yield per plant (4.07%), number of nodes per plant (4.01%), 100 seed weight (3.63%), days to 50% flowering (2.51%), whereas the remaining characteristics showed very less or careless

contribution towards divergence. Whereas, days to maturity had no contribution towards genetic divergence.

Inter and Intra Cluster Divergence D²

Table (2) displays the D² mean values within and between clusters. Eleven clusters including fifty-seven genotypes were created based on D² values. The range of intra-cluster distance was 0.00 to 175.11. The clusters that were the most divergent were clusters I, II, IV, V and XI while remaining clusters displayed zero values for intra-cluster distance. The highest intra-cluster D² value was seen in Cluster IV (D² = 175.11), which was followed by clusters XI (D² = 122.32), II (D² = 113.11), V (D² = 100.11) and cluster I (88.62). These clusters were poly-genotypic, but the remaining six clusters were mono-genotypic, showed zero value for intra-cluster divergence.

The highest inter cluster divergence was observed between genotypes of cluster V and cluster VII (899.12), followed by cluster IV and cluster V (834.87) and cluster VII and cluster IX (754.41) etc. The lowest inter cluster distance was reported between cluster VI and cluster IX (129.30).

Cluster I (88.62) was poly-genotypic and found nearest to cluster VI (129.83), while it exhibited the maximum distance with cluster V (485.47).

Cluster II (113.11) was poly-genotypic and was observed to be nearest to cluster VIII (168.03), and most distant from cluster VII (547.06).

Cluster III (0.00) was mono-genotypic and found nearest to cluster IV (145.65), while the maximum divergence was recorded with cluster V (703.85).

Cluster IV (175.11), the largest poly-genotypic cluster, was reported nearest to cluster VII (244.62) and exhibited the maximum distance with cluster V (834.87).

Cluster V (100.11) was poly-genotypic and observed nearest to cluster VIII (372.80), while it showed the maximum divergence with cluster VII (899.12).

Cluster VI (0.00) was mono-genotypic and found closest to cluster IX (129.30), while the highest inter cluster distance was recorded with cluster VII (582.51).

Cluster VII (0.00) was mono-genotypic and placed nearest to cluster XI (220.66), whereas it exhibited the maximum distance with cluster IX (754.41).

Cluster VIII (0.00) was mono-genotypic and found nearest to cluster IX (282.50), while the

maximum divergence was recorded with cluster XI (414.00).

Cluster IX (0.00) was mono-genotypic and observed nearest to cluster X (443.04), and showed the maximum inter cluster distance with cluster XI (744.35).

Cluster X (0.00) was mono-genotypic and showed minimum inter cluster distance with cluster X (215.66).

Cluster XI (122.32) was poly-genotypic.

Table 1: Contribution (%) of Different Traits towards Clustering

Source	Times ranked 1 st	Contribution %
Biological yield per plant	503	31.52
Plant height	410	25.69
Harvest index	172	10.78
Pod bearing length	99	6.20
Number of pods per plant	78	4.89
Number of effective pods per plant	74	4.64
Seed yield per plant	65	4.07
Number of nodes per plant	64	4.01
100- Seed weight	58	3.63
Days to 50% flowering	40	2.51
Number of secondary branches per plant	15	0.94
Pod length	10	0.63
Number of primary branches per plant	4	0.25
Number of effective nodes per plant	3	0.19
Number of seed per pod	1	0.06
Days to maturity	0	0

Table 2: Inter and Intra Cluster D² Value for Different Clusters

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	88.62	218.18	134.75	215.40	485.47	129.83	364.86	137.27	185.90	266.74	400.98
II		113.11	336.90	463.06	229.69	254.65	547.06	168.03	336.33	281.76	370.90
III			0.00	145.65	703.85	213.73	291.91	290.13	301.38	199.62	317.15
IV				175.11	834.87	301.00	244.62	355.59	391.47	275.89	366.94
V					100.11	462.49	899.12	372.80	502.01	595.65	601.13
VI						0.00	582.51	227.59	129.30	248.80	549.76
VII							0.00	416.86	754.41	420.20	220.66
VIII								0.00	282.50	361.09	414.00
IX									0.00	443.04	744.35
X										0.00	215.66
XI											122.32

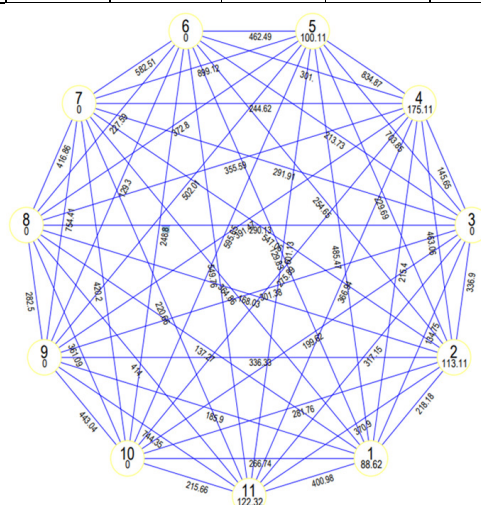


Fig. 1 : Cluster diagram

Cluster Mean for Yield and its Component Traits of Field pea Genotypes

Table (3) presents the cluster means for various yield and component traits among field pea genotypes. The analysis reveals that for days to 50% flowering, Cluster VIII exhibited the lowest mean value (56.00 days), whereas Cluster III recorded the highest mean value (70.50 days). Regarding days to maturity, Cluster VIII showed the minimum mean (96.00 days), while Cluster X had the highest mean (102.50 days). The number of primary branches per plant had the highest mean in Cluster X (2.20) and the lowest mean in Clusters VIII and IX (1.30). The number of secondary branches per plant peaked in Cluster VIII with the highest mean (6.70), and the lowest mean was recorded in Cluster III (4.00). For plant height, Cluster IV recorded the highest mean (116.24 cm), whereas Cluster V had the lowest mean (54.80 cm). The maximum mean for number of nodes per plant was found in Cluster VI (27.10), while Cluster VII recorded the lowest mean (18.20). In terms of number of effective nodes per plant, Clusters VI and IX recorded the highest mean (9.20), whereas Cluster XI showed the lowest mean value (5.67). The pod bearing length had the highest mean in Cluster IX (97.90 cm), and the lowest mean was observed in Cluster V (39.65 cm). Cluster X recorded the highest mean for number of pods per plant (12.25), while Cluster III had the lowest

mean (7.10). Similarly, the number of effective pods per plant was highest in Cluster X (13.20) and lowest in Cluster III (5.70). For pod length, Cluster VI registered the maximum mean (7.41 cm), and Cluster XI the minimum mean (5.34 cm). The number of seeds per pod was highest in Cluster VIII (5.30), while Cluster VII recorded the lowest mean (4.05). Regarding 100 seed weight, Cluster III had the highest mean value (25.90 g), and Cluster VII the lowest mean value (16.75 g). The highest mean biological yield per plant was observed in Cluster X (42.70 g), while the lowest mean was recorded in Cluster V (13.47 g). The harvest index showed the maximum mean in Cluster VI (45.11%) and the minimum mean in Cluster VII (11.59%). Finally, the seed yield per plant had the highest cluster mean in Cluster X (12.01 g), and the lowest mean value in Cluster VII (4.32 g).

Grouping of Genotypes into Various Clusters

Based on divergence research, fifty-seven genotypes of field pea were sorted into 11 cluster using Mahalanobis D² method. The genotype distributions into several clusters are shown in (Table 4) and Fig. 2 cluster number II with genotypes 19 is the largest of all the cluster after that cluster I, IV, V and clusters XI followed. Cluster III, VI, VII, VIII, IX, X consist of single genotypes.

Table 3: Cluster Mean for Yield and its Component Traits of Field pea Genotypes

Cluster	DDF	DM	NPBP	NSBP	PH	NNPP	NENPP	PBL	NPP	NEPP	PL	NSPP	100 SW	BYPP	SYPP	HI
Cluster 1	64.93	100.10	1.73	4.76	103.51	22.09	6.93	76.64	8.78	8.20	6.44	4.72	21.14	25.44	7.52	29.73
Cluster 2	66.84	100.45	1.86	4.87	69.83	18.56	7.28	76.64	8.11	8.28	6.44	4.74	20.69	21.74	7.15	33.04
Cluster 3	70.50	99.50	1.40	4.00	113.50	21.50	6.50	81.70	7.10	5.70	6.05	4.90	25.90	33.95	6.96	20.51
Cluster 4	64.73	100.18	1.95	4.85	116.24	21.11	7.85	80.16	11.29	9.94	6.08	4.71	21.49	36.79	8.06	21.76
Cluster 5	68.17	99.67	1.67	4.47	54.80	20.23	7.13	39.65	10.07	8.37	6.09	4.50	22.77	13.47	6.00	44.55
Cluster 6	69.00	101.00	1.50	5.10	97.00	27.10	9.20	67.80	11.20	13.10	7.41	5.00	24.40	26.25	11.85	45.11
Cluster 7	60.50	100.50	1.50	5.30	112.50	18.20	6.70	56.95	9.00	7.70	5.93	4.05	16.75	37.25	4.32	11.59
Cluster 8	56.00	96.00	1.30	6.70	86.20	19.10	6.20	62.00	8.15	5.90	7.11	5.30	20.10	20.85	6.67	31.97
Cluster 9	66.50	102.00	1.30	4.70	106.00	21.65	9.20	97.90	8.80	11.60	6.26	4.90	24.65	21.85	9.36	42.81
Cluster 10	70.00	102.50	2.20	5.11	67.90	21.10	8.90	54.15	12.25	13.20	6.17	4.70	23.50	42.70	12.01	28.13
Cluster 11	64.83	100.00	1.80	4.28	69.63	20.27	5.67	45.02	9.23	7.93	5.34	4.77	21.05	38.90	5.28	13.36

DDF= Days to 50% flowering, DM= Days to maturity, Plant height (cm), NPBP= Number of primary branches per plant, NSBP= Number of secondary branches per plant, NNPP= Number of nodes per plant, NENPP= Number of effective nodes per plant, PBL= Pod bearing length (cm), NPP= Number of pods per plant, NEPP= Number of effective pods per plant, PL= Pod length (cm), NSPP= Number of seeds per pod, 100 SW= 100-seed weight (g), BYPP= Biological yield per plant (g), HI= Harvest index (%), SYPP= Seed yield per plant

Table 4: Distribution of Field pea Genotypes in Different Clusters Using D² Statistics

Cluster Number	Number of genotypes	Name of genotypes
I	15	HUP-2, PantP42, IM9101, JM-6, DMR-7, HUTP2202, VL-1, PANTP574, INDIRA MATAR-1, HFP-8909, HFP2029, HFP1962, HFP 20-506, HFP-9426, SKNFP2008
II	19	HFP1904, PantP559, PantP562, Azad Pea-1, G-10, HFP529, IPFD12-2, IPFD14-2, IPFD10-12, VL-3, JAYANTI, KPMR400, IPFD1-10, DDR-44, IPFD6-3, IPFD99-13, HUDP15, HFP 20-67, HFP4
III	1	IM9102
IV	11	HFP9907B, IFP4-26, VL-46, Adarsh, PantP5, JP-180, JP885, B22, RFP 2021-1, Pant P-243, Ambika

V	3	KPMR144-1, PG3, SKNP-4-9
VI	1	Pant P-554
VII	1	VL42
VIII	1	AP2
IX	1	PANT P568
X	1	IPFD 11-5
XI	3	IPFD 23-11, IPF48, VRP-7

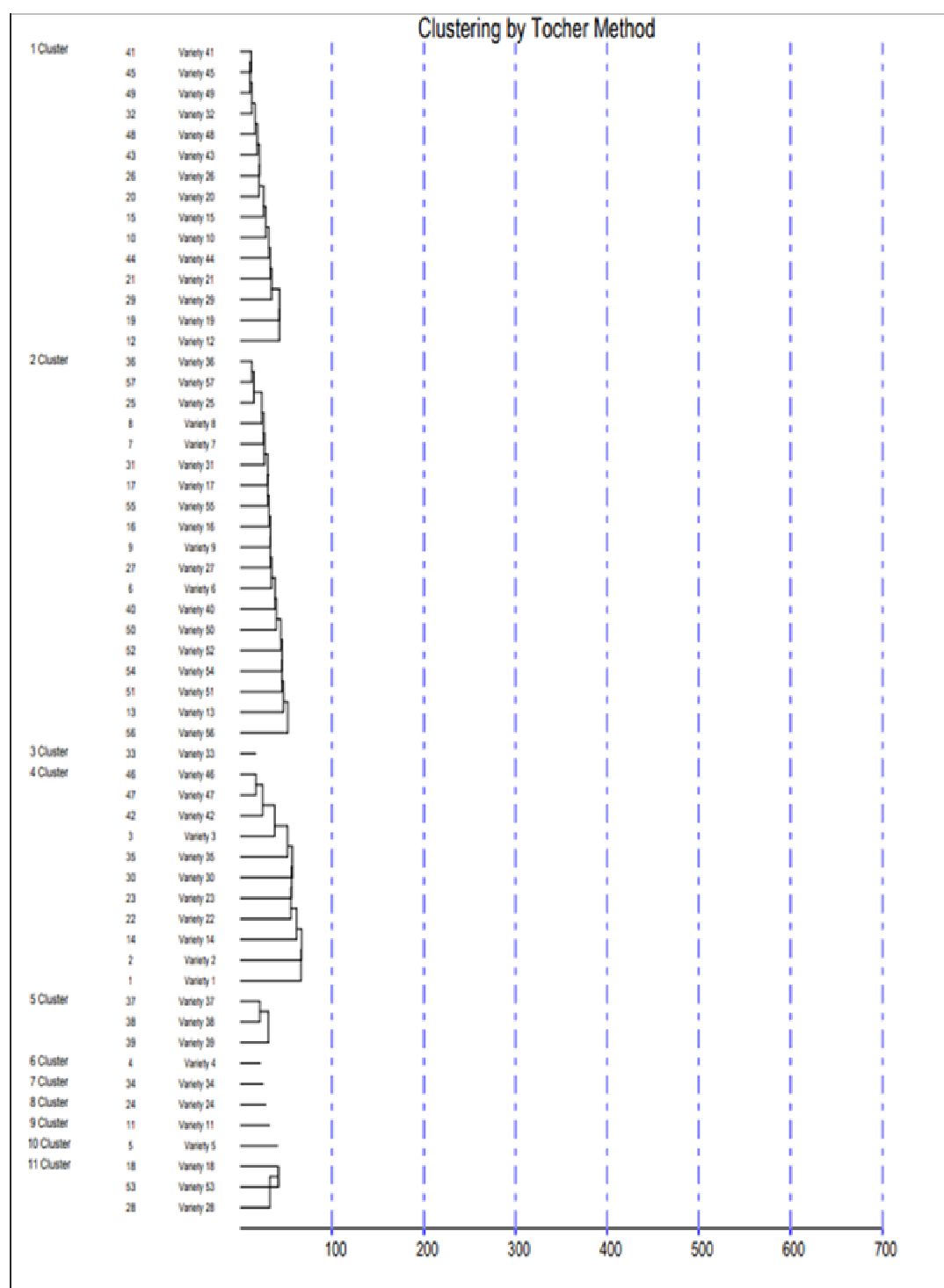


Fig. 2: Distribution of Number of Field pea Genotypes in Different Clusters Using D^2

Genetic Divergence Analysis

The present study was also aimed at analysing the genetic divergence among the fifty-seven genotypes of field pea and to identify the superior and divergent parental genotypes for formulating the crossing programme. Mahalanobis D² Statistic is a powerful tool widely used by breeders in quantifying the degree of divergence at genotypic level.

Group Constellations

Following the cluster analysis provided by Mahalanobis, the fifty-seven genotypes were grouped into eleven clusters based on D² values. While the remaining six clusters were mono-genotypic (having only one genotype each), cluster II (19), cluster I (15), cluster IV (11) and clusters V and XI (3) were poly-genotypic. The degree of diversity was further validated by the genotype clustering pattern. Eleven clusters were formed from the fifty-seven genotypes based on genetic distance.

In accordance with the current investigation, Siddika *et al.* (2014) reported five distinct clusters among 25 advanced pea lines based on 14 agronomic traits, Kanno (2016) also reported five clusters, Gupta *et al.* (2017) classified 20 pea genotypes into four clusters, Bhuvaneswari *et al.* (2017) evaluated 51 genotypes and grouped them into seven clusters, Khan *et al.* (2017) formed six clusters from the studied genotypes, Bijalwan *et al.* (2018) used Mahalanobis D² statistics to classify 23 genotypes into five clusters, Singh *et al.* (2021) reported six clusters, Kaur *et al.*

(2023) found significant genetic diversity among 24 pea genotypes grouped into five clusters.

Intra and inter cluster divergence D² values

While the remaining six clusters were mono-genotypic and had zero value for intra-cluster divergence, cluster IV displayed the greatest intra-cluster value (175.11), followed by cluster XI (122.32), cluster II (113.11), cluster V (D² = 100.11) and cluster I (88.62). Cluster V and VII genotypes showed the greatest inter-cluster difference (899.12), followed by IV and V (834.87) and Cluster VII and IX (754.41). Cluster VI and IX had the lowest reported inter-cluster distance (129.30).

Similar findings have been reported by Gupta *et al.* (2017), Bhuvaneswari *et al.* (2017), Khan *et al.* (2017), Lal *et al.* (2018), Bijalwan *et al.* (2018), Singh *et al.* (2021) and Kaur *et al.* (2023).

Per cent contribution of traits towards divergence in fifty-seven genotypes of Field pea

Following plant height, harvest index, and pod bearing length, biological yield per plant had the largest percentage contribution to divergence.

In conformity to the present investigation, Lal *et al.* (2018) for plant height, harvest index, days to 50% flowering and Kaur *et al.* (2023) for pod yield per plant.

Cluster mean values

For every feature studied, the cluster mean values displayed a large range of variation (Table 5).

Table 5: Relative Comparisons for Cluster Mean Values of Various Traits in Field Pea

S. No.	Traits	Maximum (Cluster)	Minimum (Cluster)
1	Days to 50% flowering	III	VIII
2	Days to maturity	X	VIII
3	Plant height	IV	V
4	Number of primary branches per plant	X	VIII, IX
5	Number of secondary branches per plant	VIII	III
6	Number of nodes per plant	VI	VII
7	Number of effective nodes per plant	VI, IX	XI
8	Pod bearing length	IX	V
9	Number of pods per plant	X	III
10	Number of effective pods per plant	X	III
11	Pod length	VI	XI
12	Number of seeds per pod	VIII	VII
13	100 seed weight	III	VII
14	Biological yield per plant	X	V
15	Seed yield per plant	X	VII
16	Harvest index	VI	VII

Based on the cluster mean analysis for sixteen quantitative traits in field pea, Cluster III exhibited the highest mean value for days to 50% flowering and 100 seed weight, while Cluster X recorded the highest mean for days to maturity, number of primary branches per plant, number of pods per plant, number of effective pods per plant, biological yield per plant, and seed yield per plant. Cluster IV showed superiority for plant height, whereas Cluster VIII exhibited the highest number of secondary branches per plant and the highest number of seeds per pod. Cluster VI recorded the maximum number of nodes per plant, pod length, and harvest index. The highest number of effective nodes per plant was shared by Clusters VI and IX. Cluster IX also recorded the longest pod bearing length.

Similar results and the importance of cluster-based trait analysis for parent selection were reported by Gupta *et al.* (2017), Khan *et al.* (2017), Lal *et al.* (2018), Bijalwan *et al.* (2018), Singh *et al.* (2021) and Kaur *et al.* (2023).

Conclusion

1. Since cluster V and cluster VII exhibit the greatest inter-cluster difference, crossing between their genotypes would be helpful in broadening of crop genetic base.
2. Cluster VI had the highest mean values for traits like number of secondary branches per plant, number of nodes per plant, number of effective nodes per plant, number of pods per plant, number of effective pods per plant, pod length, number of seeds per pod, 100 seed weight, harvest index and seed yield per plant.
3. Therefore, in a crossbreeding program, genotypes belonging to distant cluster may be chosen as donor parents, whose distinct traits could improve overall seed yield and other desirable traits.

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